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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   780.6
614.4
613.4
453.4
449
437.4
                                                                                         Score
                                                                                      Query
Match
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   49.7
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39.1
28.9
28.6
27.9
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BE271316 601140022
BE315016 601140772
AI743298 wg91b03 x
AI148578 qc58a11 x
AW530232 UI-R-BU0-
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REF COM	RESI BE7 LOCU DEF ACC: VERI KEYI		۵ ۵	0000000	0 0	ο	a
REFERENCE AUTHORS TITLE JOURNAL COMMENT	RESULT 1 BE741672 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	ULT 1 41672 US	33333 3444 3444 343 343 343 343 343 343	32 33 35 35	21 22 23 24 25 26	12 13 14 15 16 17 18 19	7 8 9 10
BE7411 EST. human human sym Homo : Language Mammai 1 (bi Nation Unpub Contac Email Tissu CDNA CDNA CDNA CDNA CDNA CONA CONA CONA CONA CONA CONA CONA CO	BE741672 90 N 601594724F1 NIH_MGC_9 Homo mRNA sequence. N BE741672 BE741672.1 GI:10155664 EST. human	ALIGN	198.4 12.7 273 9 AA656693 198.4 12.6 304 9 AA234133 178.6 11.4 302 9 AV169772 164.2 10.5 217 9 A1592872 159.6 10.2 576 13 B9522217 150.8 9.6 845 12 B6115475 148.4 9.5 278 17 A2326987 148.4 9.5 278 17 A2326987 148.4 9.5 278 17 A2326987 148.4 9.5 278 17 A2326987 148.4 9.5 278 14 B0781789 132 8.4 355 14 BM695109	2.4 15.4 416 10 0.2 14.7 384 12 0.2 14.7 366 12 223 14.2 402 12 2.6 14.2 402 12 0.8 13.4 345 13 0.8 13.4 353 12 8.4 13.3 222 14	5.2 21.4 424 14 1.4 21.1 363 9 6.8 20.8 490 12 0.4 20.4 322 10 0.4 18.9 317 10 6.4 18.9 417 10 6.4 18.9 417 10	04.6 25.8 600 12 401 25.5 402 9 99.4 25.4 401 9 39.7 25.3 405 9 88.8 24.8 392 10 377 24.0 378 10 354 22.5 390 14 49.2 22.2 403 14 49.8 21.6 344 10	27.6 436 9 27.0 427 9 26.2 617 12 26.1 455 9 26.0 517 12
	bp mRNA linear EST 15-SEP-2000 piens cDNA clone IMAGE:3948893 5',	NTS mRNA linear EST 15-SEP- ens cDNA clone IMAGE:3948893 5',	AA6569 AA23413 AV16977 AI59287 BJ5222 BG1154 AZ3269 AI03440 BQ78178 BM6951	N49867 AW4886 BE9484 BG30880 BF4139 BF29871 BG37500 W24884	BM9332 AIZ8893 BF5668 AW77067 BF1108 BW43377 AW222987	BG800960 0081- AI681540 tx47e0 AI1002437 or78f0 AI1193544 qe70e0 AW135577 UI-H- AW207339 UI-H- N68951 za70e12 W00630 za70e12 BE673874 7d709	AI333518 c AI621022 t BF471928 AA022949 z BF564483

FEATURES source

Location/Qualifiers
1. .903
/organism="Homo sapiens"

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BASE COUNT
ORIGIN
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TGGCCACACTCACACTCCCAGAAAACTGCATCAGAGGAATATTTTTACATGAAAAATAAG
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                                                                                                                                        CCAAGGGGCAGCCGGAGCTTCAGAAGCCCTTCAAGTACACGACGGTGACCAAGAGGTCCC
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/clone="IMAGE:3948893"
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/lab_bost="DH10B (phage-resistant)"
/lab_bost="DH10B (phage-resistant)"
/lab_bost="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: poTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5;
adaptor: GCCACCAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZaP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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93.6%;
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Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.
plate: LLCM93 row: k column: 05
High quality sequence stop: 628.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections of the 
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/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2: Closed into EcoRI/XhoI sites using the following 5;
/note-potential for accordance of the following 5;
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/db_xref="taxon:9606"
/clone="IMAGE:3049468"
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Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 639)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. CONSOTTIUM (LLNL) DNA Sequencing by: Incytte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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                                               /note="Organ: ovary; Vector: pOTB); Site_1: XhoI; Site_1: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit
                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_9"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
               (Stratagene) and Superscript II RT (Life Technologies)." 194 \text{ c} 199 \text{ g} 98 \text{ t}
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 455)
1 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL Cancer Institute, Cancer Genome Anatomy Promational Cancer Institute,
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 561 Std Error: 0.00
                                                              National Cancer Institute,
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                AI743298 455 bp mRNA linear EST wg91b03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDN/IMAGE:2372429 3' similar to TR:076093 076093 FIBROBLAST
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                                                        449 bp mRNA linear | qc58a11.x1 Soares_placenta_8to9weeks_2NbHP8to9w Homo clone IMAGE:1713788 3', mRNA sequence
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/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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                                                                                                                               AAGGATTTTATTGTTGACTTGAAACCCCCGATGACAAAAGACTCACGCAAAGGGACTGTA 1399
                                                                                                                                                                                       TGTACATTGTGTTTAAAAGAAGACAAAAACTGAACCAAAACTCTTGGGGGGAGGGGTGAT 1339
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                                                       GTCAACCCACAGGTGCTTGTCTCTCTCTAGGAACAGACACTCTAAACTCGTCCCCAGAG
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 538 Std Error: 0.00
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Contact: Robert Strausberg, Ph.D.
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National Cancer Institute, Cancer Genome Anat
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/db_xref="taxon:9606"
/clone="IMAGE:1713788"
/clone="IMAGE:1713788"
/clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
/dev_stage="two placentae: one from 8 weeks and ar
from 9 weeks post conception"
/lab_host="DH10B (ampicillin resistant)"
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CCAGACGCGGGCTCGGGACGATGTGAGCCGTAAGCAGCTGCGGCTGTACCAGCTCTACAG
                                                             CTTCCAGGTACAGGTGCTGGTTGCCGAGGAGAACGTGGACTTCCGCATCCACGTGGAGAA
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                                      CTTCCAGGTTCAGGTGTTGGCAGCCGAGGAGAACGTGGACTTCCGCATCCATGTGGAGAA
                                                                                                                        CGCGATGTATTCAGCGCCCTCCGCCTGCACTTGCCTGTGTTTACACTTTCTACTGCTGTG
                                                                                                                                                                                                       Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of seque
is likely internal to the messer cDNA Library Preparation: M.E
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com) The following repetitive
elements were found in this cDNA sequence: 39-64,
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451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus
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UI-R-BU0-amu-b-08-0-UI.sl UI-R-BU0 Rattus norvegicus
UI-R-BU0-amu-b-08-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DHIOB (Life Technologies)"
//lab_host="DHIOB (Life Technologies)"
//note="Vector: pT733D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BUO
library is a subtracted library derived from a mixture of
eye and ganglia tissues. For a detailed description of the
library from which this clone was derived, please visit
our web site at ratest-eng.uiowa.edu. The subtraction has
been previously described in (Bonaldo, Lennon and Soares,
been Research 6:791-806, 1996)
                                                                                                                                                                                                                                                                                                                                                                                         TAG_TISSUE=spleen
TAG_SEQ=GAGA"
139 c 164 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAG_LIB=UI-R-BUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="UI-R-BU0-amu-b-08-0-UI"
/clone_lib="UI-R-BU0"
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/db_xref="taxon:10116"
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91.8%;
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                                                                                                                                                                                                                                                                                          Mismatches
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 436)
1 (CI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI333518 436 bp mRNA qp96a07.x1 Soares_fetal_lung_NbHL19W Ho
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               133
                                                         double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed
                                                                                                                                                          Soares and M.Fatima Bonaldo. This library was construct from the same fetus as the fetal heart library, Soares fetal heart NbH19w."

120 c 97 g 86 t
                                                                                                                                                                                                                                                          /clone_lib="Soares_fetal_lung_NbHL19W"
                                                                                                                                                                                                                                                                           /clone="IMAGE:1930836"
                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                           /dev_stage="19 weeks"
                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens'
                                                                                                                                                                                                                                                                                                                                                           Gibco.
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Query Match Best Local

Similarity

27.6%;

Score 432.8; DB Pred. No. 2e-49;

9;

Conservative

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Mismatches

Length Indels

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Gaps

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                                                                                                       www-bio.llnl.gov/bbrp/image/image.html
Seg primer: -40UP from Gibco.
    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            sequence.
AI621022
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI621022 427 bp mRNA linear EST 21-APR-1999 ts76all.xl NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237180 3' similar to TR:076093 076093 FIBROBLAST GROWTH FACTOR 18. ;, mRNA
                                                                                                                                                                                                 Bonaldo, Ph.D.
                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                           Tissue Procurement: Christopher A. Moskaluk, M.D., R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                Unpublished (1997)
                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 427)
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                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL
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                                                                                                                                                                      cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome
                                                                                                                                                                                                              cDNA Library Preparation: M.
                                                                                                                                                                                                                                                                                            Gene Index
                                                                                                                                             distribution: NCI-CGAP clone distribution through the I.M.A.G.E. Consortium/LLNL at:
                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2237180"
/clone_lib="NCI_CGAP_GC6"
  /note="Vector:
             /tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
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1315 CAAAACTCTTGGGGGGGAGGGTGATAAGGATTTTATTGTTGACTTGAAACCCCCCGATGAC
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425; Conserv
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Pred. No. 2.8e
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BF471928 617 bp mRNA 1 UI-M-BH3-awr-c-01-0-UI.r1 NTH_BMAP_M_S4 Mus UI-M-BH3-awr-c-01-0-UI 5', mRNA sequence. BF471928 BF471928.1 GI:11541111 20892-9643, USA Tel: 301 443 1706 Fax: 301 443 9890 Mus musculus Eukaryota; M 6001 Executive Blvd. 20892-9643, USA Contact: Chin, H
National Institute of Mental Health 97044477 Genome Res. 6 (9), discovery Normalization and subtraction: Bonaldo, M.F., Mammalia; Eutheria; Rodentia; Sciurognathi; 1 (bases 1 to 617) house mouse Metazoa; Lennon, G. and Soares, M.B. 791-806 Chordata; Craniata; Vertebrata; Rodentia; Sciurognathi; Muridae; 7N-7190, MSC (1996) CWO approaches 9643, linear musculus Bethesda, 6 facilitate Euteleostomi; EST 04-DEC-2000 Murinae; ¥ clone

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BASE COUNT
ORIGIN
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                       ACCAGCAAGGAGTGTGTGTCATCGAGAAGGTTCTGGAGAACAACTACACGGCCCTGATG 975
                                                                                                                                                             GAGACGGAATTCTACCTGTGCATGAACCGCAAAGGCAAGCTCGTGGGGAAGCCCGATGGC 915
                                                                                                                                                                                                                                                                                              TATGCCCAGCTCCTAGTGGAGACAGACACCTTCGGTAGTCAAGTCCGGATCAAGGGCAAG 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTCGGGACGATGTGAGCCGTAAGCAGCTGCGGCTGTACCAGCTCTACAGCCGGACCAGT 735
                                                                                                                                                                                                                                                         TATGCCCAGCTCCTAGTGGAGACAGATACCTTCGGGAGTCAAGTCCGGATCAAGGGCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTCGAGATGATGTGAGTCGGAAGCAGCTGCGCTTGTACCAGCTCTATAGCAGGACCAGT 219
                                                                                                                                                                                                                                                                                                                                                                                          GGGAAGCACATTCAAGTCCTGGGCCGTAGGATCAGTGCCCGTGGCGAGGACGGGGACAAG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                collaborative arrangements Seq primer: M13 Reverse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: M.B. Soares Lab Clone distribution:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153
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//dev_stage="73-32 days"
//dev_stage="73-32 days"
//dev_stage="73-32 days"
//lab_bost="PH10B (Life Technologies)"
//note="vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_M_S4 library is a subtracted library of a series,
ultimately derived from a mixture of individually tagged
normalized libraries from ten regions of the mouse brain
(cerebellum, brain stems, olfactory bulbs, hypothalamus,
cortex, amygdala, basal ganglia, pineal gland, striatum,
hipoccampus) after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
generated in this process: NIH_BMAP_M_S3.1,
NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.2,
NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1,
NIH_BMAP_M_S4) was constructed as follows: PCRamplified
cDNA inserts from NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and
NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived
was used as a driver in a hybridization with a pool of
the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1
libraries in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library)
was purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B harteria, (lifemechanlogies) to generate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      into DH10B bacteria (LifeTechnologies) to generate the NIH_BMAP_M_S4 library. This procedure has been previous described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)"

a 157 c 194 g 110 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="UI-M-BH3-awr-c-01-0-UI"
/clone_lib="NIH_BMAP_M_S4"
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Pred. No. 1.3e-46;
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Вp

Qy Дb δÃ В Qy

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Query Match
Best Local Similarity

26.1%; 98.9%;

Score 409.8; DB 9; Pred. No. 2.5e-46;

Length 455

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VERSION
KEYWORDS
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AA022949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 557 Std Error: 0.00 Seq primer: -40M13 fwd. from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 455)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
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/db_xref="GDB:1281267"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares_fetal_heart_NbHH19W"
                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:364563"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         444;
                                                                                                                   Email: msoares@blue.weeg.uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen
This clone is also available through the I.M.A.G.E. Consortiu
                                                                                                                                                                            Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                      Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                             BF564483 517 bp mRNA UI-R-BUO-amu-b-08-0-UI.rl UI-R-BUO Rattus UI-R-BUO-amu-b-08-0-UI 5', mRNA sequence.
                                                                                               Seq
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Bonaldo, M.F., Lenno
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                                                                                               primer: M13 Forward
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 /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BUO-amu-b-08-0-UI"
/clone_lib="UI-R-BUO"
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a 134 c 140 g 133 t 1 others
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Mu, X., Zhao, S., Pershad, R., Hsieh, T.-F., Scarpa, A., Wang, S.W., Mu, X., Zhao, S., Pershad, P.D., Thomas, T.L., Gan, L. and Klein, W.H.
                                                                                                                                                                                                                                                                                    BG800960
0081-34 Mouse
                    and microarray analysis
                                 White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. Gene expression in the developing mouse retina
                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                             Mus musculus
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Fax: 713 790 0329.
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                                                                     AAGAGGTCCCGTCGGATCCCGGCCCACACACCCTGCCTAGGCCACCCCGCCGCCGCCGCCTC 1194
                   AAAAATAAGGAAGAAGCTCTATTTTTGTACATTGTGTTTTAAAAGAAGACAAAAACTGAAC 1314
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 AGGTCGCCCTGGCCACACTCACACTCCCAGAAAACTGCATCAGAGGAATATTTTTACATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
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Unpublished (1997)
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Seq primer: -40UP from Gibco.
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National Cancer Institute, Cancer Genome Ana
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a 110 c 95 g 76 t 1 others
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/lab_host="DH10B"
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                 AAAAATAAGGAAGAAGCTCTATTTTGTACATTGTGTTTAAAAGAAGACAAAAAACTGAAC
                                                                                                                                                                 AAGAGGTCCCGTCGGATCCGGCCCACACACCCTGCCTAGGCCACCCCGCCGCGGCCCCTC 1194
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                                                     AGGTCGCCCTGGCCACACTCACACTCCCAGAAAACTGCATCAGAGGAATATTTTTACATG
                                                                                        AGGTCGCCCTGGCCACACTCACACTCCCAGAAAACTGCATCAGAGGAATATTTTTACATG 1254
400;
                                                                                                                                                www-bio.lini.gov/bbrp/image/image.html
Insert Length: 841 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Onpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher M
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae, 1 (bases 1 to 401)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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or78f08.s1 NCI_CGAP_Lu5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-GAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="carcinoid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:1601991"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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99.8%;
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Pred. No. 6.8e-45;
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BE:1601991 3',
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                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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               25.3%;
98.8%;
Score 397; DB
Pred. No. 1.4e
0; Mismatches
               DB 9;
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